

WO 01/09305

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> PURINE METABOLISM GENES IN PLANTS

<130> BB-1386-Pl

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<150> BB1386 US PRV

<151> 1999-07-30

<160> 24

<170> Microsoft Office 97

<210> 1

<211> 1910

<212> DNA

<213> Zea mays

<400> 1

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<212> PRT

<213> Zea mays

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 Thr Phe Phe Thr Asp Leu His Tyr Ile Leu Arg Val Thr Ala Ala Gly
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 Lys Thr Ala Pro His Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr
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 Ser Ala Ser Lys Tyr Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly
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 Arg Lys Gln Ser Glu Trp Asp Gln Leu Ala Ser Trp Ile Val Asn Asn
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 305 310 315 320

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Ser His Pro Gln Leu His Val Phe Leu Lys Gln Val Val Gly Leu Asp
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Leu Val Asp Asp Glu Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met
 340 345 350

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Tyr Ala Tyr Tyr Cys Tyr Ala Asn Leu Phe Thr Leu Asn Lys Leu Arg
 370 375 380

Glu Ser Lys Gly Met Thr Thr Ile Lys Phe Arg Pro His Ala Gly Glu
 385 390 395 400

Ala Gly Asp Val Asp His Leu Ala Ala Thr Phe Leu Leu Cys His Asn
 405 410 415

Ile Ser His Gly Ile Asn Leu Arg Lys Ser Pro Val Leu Gln Tyr Leu
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Tyr Tyr Leu Gly Gln Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn
 435 440 445

Ser Leu Phe Leu Asp Tyr His Arg Asn Pro Phe Pro Thr Phe Phe Gln
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Arg Gly Leu Asn Val Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His
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Leu Thr Lys Glu Pro Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Leu
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Trp Lys Leu Ser Ser Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val
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Tyr Gln Ser Gly Phe Ser His Ala Leu Lys Ala His Trp Ile Gly Lys
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Val Pro His Ile Arg Val Gln Phe Arg Glu Met Ile Trp Arg Asn Glu
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 <213> Oryza sativa

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 35 40 45
 Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu
 50 55 60
 Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr Tyr Leu
 65 70 75 80
 Thr Leu Lys Glu Val Phe Glu Ser Leu Asp Leu Thr Gly Tyr Asp Leu
 85 90 95
 Asn Val Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe His Arg
 100 105 110
 Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser Arg Leu
 115 120 125

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Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg Phe Leu
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Ala Glu Leu Thr Lys Glu Val Phe Ser Asp Leu Glu Ala Ser Lys Tyr
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Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Lys Ser Glu
 165 170 175

Trp Asp Gln Met Ala Ser Trp Ile Val Asn Asn Glu Leu Tyr Ser Glu
 180 185 190

Asn Val Val Trp Leu Ile Gln Ile Pro Arg Ile Tyr Asn Val Tyr Arg
 195 200 205

Glu Met Gly Thr Ile Asn Ser Phe Gln Asn Leu Leu Asp Asn Ile Phe
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Leu Pro Leu Phe Glu Val Thr Val Asp Pro Ala Ser His Pro Gln Leu
 225 230 235 240

His Val Phe Leu Gln Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu
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Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Gln
 260 265 270

Trp Thr Asn Val Phe Asn Pro Ala Tyr Ala Tyr Tyr Val Tyr Tyr Cys
 275 280 285

Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met
 290 295 300

Thr Thr Ile Lys Leu Arg Pro His Cys Gly Glu Ala Gly Asp Ile Asp
 305 310 315 320

His Leu Ala Ala Ala Phe Leu Thr Ser His Asn Ile Ala His Gly Val
 325 330 335

Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Ala Gln
 340 345 350

Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn Ser Met Phe Ile Asp
 355 360 365

Tyr His Arg Asn Pro Phe Pro Thr Phe Phe Leu Arg Gly Leu Asn Val
 370 375 380

Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys Glu Pro
 385 390 395 400

Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Leu Trp Lys Leu Ser Ser
 405 410 415

Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val Tyr Gln Ser Gly Phe
 420 425 430

Ser His Arg Leu Lys Ser His Trp Ile Gly Arg Asn Tyr Tyr Lys Arg
 435 440 445

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Gly His Asp Gly Asn Asp Ile His Gln Thr Asn Val Pro His Ile Arg
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 <213> Glycine max

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 His Val His His Ser Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe
 35 40 45
 Ile Lys Ser Lys Leu Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg
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 Asp Gly Thr Tyr Leu Thr Leu Glu Glu Val Phe Lys Ser Leu Asp Leu
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 35 40 45
 Arg Leu Tyr Asn Val Tyr Gln Xaa Lys Trp Gly Leu Leu His His Phe
 50 55 60
 Lys Asn Phe Leu Gly Gln His Phe Pro Pro Pro Val Trp Arg Leu Leu
 65 70 75 80

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Xaa Ser Ser Ser His Pro Ala Leu His Val Phe Pro Lys Ala Gly Leu
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Gly Leu Asp Leu Val Asp Asp Glu Xaa Asn Leu
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 <213> Zea mays

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Ile Ala Leu Pro Asp
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 Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu Arg Lys
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 Pro Phe Tyr Tyr Glu Gln Gln Thr Lys Thr Glu His His Phe Glu Met
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 Val Asp Gly Val Ile His Val Tyr Pro Asn Lys Asp Ala Lys Glu Arg
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 Asp Leu His Gly Val Gln Pro Asp Pro Ile Ala Ala Asp Ile Leu Arg
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 Lys Glu Pro Glu His Glu Thr Phe Thr Arg Leu Arg Ile Thr Pro Leu
 65 70 75 80
 Glu Ala Pro Ser Pro Asp Glu Ile Glu Ala Tyr Val Val Leu Gln Glu
 85 90 95
 Cys Leu Glu Met Arg Lys Arg Tyr Val Phe Arg Glu Ala Val Ala Pro
 100 105 110
 Trp Asp Lys Glu Val Ile Ser Asp Pro Ser Thr Pro Lys Pro Asn Pro
 115 120 125
 Asp Pro Phe Leu Tyr Ile Pro Glu Gly Asn Ser Asp His Tyr Phe Glu
 130 135 140
 Met Gln Asp Gly Val Ile Arg Val Tyr Pro Asp Arg Asp Ala Lys Glu
 145 150 155 160
 Glu Leu Phe Pro Val Ala Asp Ala Thr Thr Phe Phe Thr Asp Leu His
 165 170 175
 His Leu Leu Arg Val Ile Ala Ala Gly Asn Ile Arg Thr Leu Cys His
 180 185 190
 His Arg Leu Asn Leu Leu Glu Gln Lys Phe Asn Leu His Leu Met Leu
 195 200 205
 Asn Ala Asp Arg Glu Phe Leu Ala Gln Lys Ser Ala Pro His Arg Asp
 210 215 220
 Phe Tyr Asn Val Arg Lys Val Asp Thr His Val His His Ser Ala Cys
 225 230 235 240
 Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu Arg Lys
 245 250 255
 Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr Tyr Leu Thr Leu
 260 265 270
 Glu Glu Val Phe Lys Ser Leu Asp Leu Ser Gly Tyr Asp Leu Asn Val
 275 280 285
 Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe His Arg Phe Asp
 290 295 300
 Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser Arg Leu Arg Glu
 305 310 315 320
 Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg Phe Leu Gly Glu
 325 330 335
 Leu Thr Lys Gln Val Phe Ser Asp Leu Ala Ala Ser Lys Tyr Gln Met
 340 345 350

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Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Gln Ser Glu Trp Asp
355 360 365

Gln Leu Ala Ser Trp Ile Val Asn Asn Asp Leu Tyr Ser Glu Asn Val
370 375 380

Val Trp Leu Ile Gln Leu Pro Arg Leu Tyr Asn Val Tyr Lys Glu Met
385 390 395 400

Gly Ile Val Thr Ser Phe Gln Asn Met Leu Asp Asn Ile Phe Ile Pro
405 410 415

Leu Phe Glu Val Thr Val Asn Pro Asp Ser His Pro Gln Leu His Val
420 425 430

Phe Leu Lys Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu Ser Lys
435 440 445

Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Gln Trp Thr
450 455 460

Asn Val Phe Asn Pro Ala Phe Ser Tyr Tyr Val Tyr Tyr Cys Tyr Ala
465 470 475 480

Asn Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met Thr Thr
485 490 495

Ile Lys Phe Arg Pro His Ser Gly Glu Ala Gly Asp Ile Asp His Leu
500 505 510

Ala Ala Thr Phe Leu Thr Ala His Asn Ile Ala His Gly Ile Asn Leu
515 520 525

Lys Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Ala Gln Ile Gly
530 535 540

Leu Ala Met Ser Pro Leu Ser Asn Asn Ser Leu Phe Leu Asp Tyr His
545 550 555 560

Arg Asn Pro Phe Pro Met Phe Phe Leu Arg Gly Leu Asn Val Ser Leu
565 570 575

Ser Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys Glu Pro Leu Val
580 585 590

Glu Glu Tyr
595

<210> 19

<211> 1988

<212> DNA

<213> Triticum aestivum

<400> 19

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tcaaaaagga	tttatcctgt	ttgctgatgc	acgagacctt	tttcaccgac	ttacattatg	180
ttctccgggt	gactgccgcg	gggaacacaa	gaactgtctg	ccataaccga	ttgaatcttc	240
tagaacataa	gttcaaattt	catctgatgt	taaacgcgga	cagggagttt	cttgcccaaa	300

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ctgatgaggt tgtcattttc agagatggta catatatgac tttgaaggag gtttttgaga 480
gcttggaactt aactgggtat gacttgaatg ttgatttgct agatgtccat gcggacaaaa 540
gtacgtttca tcgttttgac aaattcaacc ttaaatacaa tccatgtgga caaagtaggc 600
tacgggagat tttccttaaa caggacaatc ttattcaagg acgatttctt gctgagctga 660
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cagggaggca agtgctcggt gtgaaactgt cgcccttttc gcctgtaaag gattgtaatt 1920
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<210> 20

<211> 345

<212> PRT

<213> Triticum aestivum

<400> 20

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Arg Cys Lys Phe Phe Ser Asp Leu Asn Ala Ser Lys Tyr Gln Met Ala
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Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Gln Ser Glu Trp Asp Gln
      20              25              30
Leu Ala Ser Trp Ile Val Asn Asn Glu Leu Tyr Ser Glu Asn Val Val
      35              40              45
Trp Leu Ile Gln Ile Pro Arg Leu Tyr Asn Val Tyr Gln Gln Met Gly
      50              55              60
Ile Val Thr Ser Phe Gln Asn Leu Leu Asp Asn Ile Phe Leu Pro Leu
      65              70              75              80
Phe Glu Val Thr Ile Asp Pro Ala Ser His Pro Gln Leu His Val Phe
      85              90              95
Leu Lys Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu Ser Lys Pro
      100              105              110
Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Glu Trp Thr Asn
      115              120              125

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Val Phe Asn Pro Ala Phe Ser Tyr Tyr Ala Tyr Tyr Cys Tyr Ala Asn
130 135 140

Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met Asn Thr Ile
145 150 155 160

Lys Phe Arg Pro His Ala Gly Glu Ala Gly Asp Val Asp His Leu Ala
165 170 175

Ala Thr Phe Leu Leu Cys His Ser Ile Ser His Gly Ile Asn Leu Arg
180 185 190

Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Gly Gln Ile Gly Leu
195 200 205

Ala Met Ser Pro Leu Ser Asn Asn Ser Leu Phe Leu Asp Tyr His Arg
210 215 220

Asn Pro Phe Pro Met Phe Phe Gln Arg Gly Leu Asn Val Ser Leu Ser
225 230 235 240

Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys Glu Pro Leu Val Glu
245 250 255

Glu Tyr Ser Ile Ala Ala Ser Leu Trp Lys Leu Ser Ser Cys Asp Leu
260 265 270

Cys Glu Ile Ala Arg Asn Ser Val Tyr Gln Ser Gly Phe Ser His Ala
275 280 285

Leu Lys Ala His Trp Ile Gly Lys Asn Tyr Tyr Lys Arg Gly Pro Ser
290 295 300

Gly Asn Asp Ile His Arg Thr Asn Val Pro Thr Ile Arg Ile Glu Phe
305 310 315 320

Arg Asp Leu Ile Trp Arg Asp Glu Met Gln Leu Val Tyr Leu Asn Asn
325 330 335

Val Ile Leu Pro Asp Glu Val Asp Gln
340 345

<210> 21
<211> 1447
<212> DNA
<213> Glycine max

<400> 21
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gtatttcttc aagattacaa acagattatt gcagctcgaa cagggccaat cgaagcatac 120
ggagtaatac atttactttg caatctcgag tccttcacac aaaatctttt caatacaata 180
aatcaaaatg tgtggtgaaa atatgaagca gttcctcaag gagctcccaa aatgtgagca 240
tcacattcat atcgaggggt ctctgtctcc agctctgctg ttcgaattgg caaagacaaa 300
caacatcgcc cttcccgact ctgcggtga tgccctcttc aaatctcccc aagaactcga 360
gtctcgctac gaacggttta ctctctcaa cgatttcctc cattactatt acattggcat 420
gtcagtgtta ataaaccctg ccgactatga aagcttgaggc tatgaatata tcacaaaagc 480
aaatcgcgac ggtgttcacc atgctgaaat tttcttcgat ccacaagcac aactgaacg 540
tggaattgca tacaacactg ttgttgaggg tctttcgggt ggactaaagc gcgctgagaa 600

WO 01/09305

PCT/US00/21009

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ggatttttgggt atcacctcaa aactcattct atgctttttg cgacacttgt cggctgagga 660
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aaaaaaaaa 1447

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<210> 22

<211> 355

<212> PRT

<213> Glycine max

<400> 22

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Met Cys Gly Glu Asn Met Lys Gln Phe Leu Lys Glu Leu Pro Lys Cys
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Glu His His Ile His Ile Glu Gly Ser Leu Ser Pro Ala Leu Leu Phe
      20              25              30

Glu Leu Ala Lys Thr Asn Asn Ile Ala Leu Pro Asp Ser Ala Ala Asp
      35              40              45

Ala Ser Phe Lys Ser Pro Gln Glu Leu Glu Ser Arg Tyr Glu Arg Phe
      50              55              60

Thr Ser Leu Asn Asp Phe Leu His Tyr Tyr Tyr Ile Gly Met Ser Val
      65              70              75              80

Leu Ile Asn Pro Ala Asp Tyr Glu Ser Leu Ala Tyr Glu Tyr Leu Thr
      85              90              95

Lys Ala Asn Arg Asp Gly Val His His Ala Glu Ile Phe Phe Asp Pro
      100              105              110

Gln Ala His Thr Glu Arg Gly Ile Ala Tyr Asn Thr Val Val Glu Gly
      115              120              125

Leu Ser Ala Gly Leu Lys Arg Ala Glu Lys Asp Phe Gly Ile Thr Ser
      130              135              140

Lys Leu Ile Leu Cys Phe Leu Arg His Leu Ser Ala Glu Asp Ala Lys
      145              150              155              160

Thr Thr Tyr Gln Glu Ala Val Ser Leu Gly His Phe Ser Asn Gly Thr
      165              170              175

Val Ala Ala Ile Gly Leu Asp Ser Ser Glu Val Gly Phe Pro Pro Glu
      180              185              190

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WO 01/09305-

Ile Phe Arg Glu Ile Tyr Glu Ser Ala Glu Thr Lys Gly Ile His Arg
195 200 205

Thr Ala His Ala Gly Glu Glu Gly Asp Thr Ser Tyr Ile Ser Arg Ala
210 215 220

Leu Asp Ile Cys Lys Val Glu Arg Ile Asp His Gly Ile Arg Leu Ala
225 230 235 240

Glu Asp Glu Asn Leu Leu Lys Arg Val Ala Glu Gln Gly Thr Met Leu
245 250 255

Thr Val Cys Pro Leu Ser Asn Val Arg Leu Arg Cys Val Glu Asn Val
260 265 270

Gly Gln Leu Pro Ile Arg Lys Phe Leu Asp Gly Gly Ile Lys Phe Ser
275 280 285

Ile Asn Ser Asp Asp Pro Ala Tyr Phe Gly Gly Tyr Ile Leu Asp Asn
290 295 300

Tyr Leu Ala Val Gln Glu Ala Phe Gly Leu Asn Leu Lys Glu Trp Lys
305 310 315 320

Tyr Ile Ala Thr Ser Ala Ile Glu Gly Ser Trp Cys Asp Asp Glu Arg
325 330 335

Lys Ala Val Leu Leu Ser Lys Val Asp Ala Cys Ala Lys Lys Tyr Glu
340 345 350

Ala Leu Leu
355

<210> 23
<211> 600
<212> PRT
<213> [Arabidopsis thaliana]

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Cys Leu Gln Glu Cys Leu Glu Leu Arg Lys Arg Tyr Val Phe Gln Glu
20 25 30

Thr Val Ala Pro Trp Glu Lys Glu Val Ile Ser Asp Pro Ser Thr Pro
35 40 45

Lys Pro Asn Thr Glu Pro Phe Ala His Tyr Pro Gln Gly Lys Ser Asp
50 55 60

His Cys Phe Glu Met Gln Asp Gly Val Val His Val Phe Ala Asn Lys
65 70 75 80

Asp Ala Lys Glu Asp Leu Phe Pro Val Ala Asp Ala Thr Ala Phe Phe
85 90 95

Thr Asp Leu His His Val Leu Lys Val Ile Ala Ala Gly Asn Ile Arg
100 105 110

WO 01/09305

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Thr Leu Cys His Arg Arg Leu Val Leu Leu Glu Gln Lys Phe Asn Leu
 115 120 125
 His Leu Met Leu Asn Ala Asp Lys Glu Phe Leu Ala Gln Lys Ser Ala
 130 135 140
 Pro His Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr His Val His
 145 150 155 160
 His Ser Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser
 165 170 175
 Lys Leu Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr
 180 185 190
 Tyr Leu Thr Leu Arg Glu Val Phe Glu Ser Leu Asp Leu Thr Gly Tyr
 195 200 205
 Asp Leu Asn Val Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe
 210 215 220
 His Arg Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser
 225 230 235 240
 Arg Leu Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg
 245 250 255
 Phe Leu Gly Glu Ile Thr Lys Gln Val Phe Ser Asp Leu Glu Ala Ser
 260 265 270
 Lys Tyr Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Met
 275 280 285
 Ser Glu Trp Asp Gln Leu Ala Ser Trp Ile Val Asn Asn Asp Leu Tyr
 290 295 300
 Ser Glu Asn Val Val Trp Leu Ile Gln Leu Pro Arg Leu Tyr Asn Ile
 305 310 315 320
 Tyr Lys Asp Met Gly Ile Val Thr Ser Phe Gln Asn Ile Leu Asp Asn
 325 330 335
 Ile Phe Ile Pro Leu Phe Glu Ala Thr Val Asp Pro Asp Ser His Pro
 340 345 350
 Gln Leu His Val Phe Leu Lys Gln Val Val Gly Phe Asp Leu Val Asp
 355 360 365
 Asp Glu Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro
 370 375 380
 Ala Gln Trp Thr Asn Ala Phe Asn Pro Ala Phe Ser Tyr Tyr Val Tyr
 385 390 395 400
 Tyr Cys Tyr Ala Asn Leu Tyr Val Leu Asn Lys Leu Arg Glu Ser Lys
 405 410 415
 Gly Met Thr Thr Ile Thr Leu Arg Pro His Ser Gly Glu Ala Gly Asp
 420 425 430

WO 01/09305.

PCT/US00/21009

Ile Asp His Leu Ala Ala Thr Phe Leu Thr Cys His Ser Ile Ala His
 435 440 445

Gly Ile Asn Leu Arg Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu
 450 455 460

Ala Gln Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn Ser Leu Phe
 465 470 475 480

Leu Asp Tyr His Arg Asn Pro Phe Pro Val Phe Phe Leu Arg Gly Leu
 485 490 495

Asn Val Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys
 500 505 510

Glu Pro Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Val Trp Lys Leu
 515 520 525

Ser Ala Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val Tyr Gln Ser
 530 535 540

Gly Phe Ser His Ala Leu Lys Ser His Trp Ile Gly Lys Asp Tyr Tyr
 545 550 555 560

Lys Arg Gly Pro Asp Gly Asn Asp Ile His Lys Thr Asn Val Pro His
 565 570 575

Ile Arg Val Glu Phe Arg Asp Thr Val Trp Asn Glu Ile Tyr Leu Phe
 580 585 590

Phe Thr Gln Val Asn Phe Ser Leu
 595 600

<210> 24
 <211> 333
 <212> PRT
 <213> [Escherichia coli]

<400> 24
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Gly Asn Ile Arg Pro Gln Thr Ile Leu Glu Leu Gly Arg Gln Tyr Asn
 20 25 30

Ile Ser Leu Pro Ala Gln Ser Leu Glu Thr Leu Ile Pro His Val Gln
 35 40 45

Val Ile Ala Asn Glu Pro Asp Leu Val Ser Phe Leu Thr Lys Leu Asp
 50 55 60

Trp Gly Val Lys Val Leu Ala Ser Leu Asp Ala Cys Arg Arg Val Ala
 65 70 75 80

Phe Glu Asn Ile Glu Asp Ala Ala Arg His Gly Leu His Tyr Val Glu
 85 90 95

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Leu Arg Phe Ser Pro Gly Tyr Met Ala Met Ala His Gln Leu Pro Val
 100 105 110

Ala Gly Val Val Glu Ala Val Ile Asp Gly Val Arg Glu Gly Cys Arg
 115 120 125

Thr Phe Gly Val Gln Ala Lys Leu Ile Gly Ile Met Ser Arg Thr Phe
 130 135 140

Gly Glu Ala Ala Cys Gln Gln Glu Leu Glu Ala Phe Leu Ala His Arg
 145 150 155 160

Asp Gln Ile Thr Ala Leu Asp Leu Ala Gly Asp Glu Leu Gly Phe Pro
 165 170 175

Gly Ser Leu Phe Leu Ser His Phe Asn Arg Ala Arg Asp Ala Gly Trp
 180 185 190

His Ile Thr Val His Ala Gly Glu Ala Ala Gly Pro Glu Ser Ile Trp
 195 200 205

Gln Ala Ile Arg Glu Leu Gly Ala Glu Arg Ile Gly His Gly Val Lys
 210 215 220

Ala Ile Glu Asp Arg Ala Leu Met Asp Phe Leu Ala Glu Gln Gln Ile
 225 230 235 240

Gly Ile Glu Ser Cys Leu Thr Ser Asn Ile Gln Thr Ser Thr Val Ala
 245 250 255

Glu Leu Ala Ala His Pro Leu Lys Thr Phe Leu Glu His Gly Ile Arg
 260 265 270

Ala Ser Ile Asn Thr Asp Asp Pro Gly Val Gln Gly Val Asp Ile Ile
 275 280 285

His Glu Tyr Thr Val Ala Ala Pro Ala Ala Gly Leu Ser Arg Glu Gln
 290 295 300

Ile Arg Gln Ala Gln Ile Asn Gly Leu Glu Met Ala Phe Leu Ser Ala
 305 310 315 320

Glu Glu Lys Arg Ala Leu Arg Glu Lys Val Ala Ala Lys
 325 330